

A1 comparison program NCBI-BLAST2 (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from www-ncbi.nlm.nih.gov or otherwise obtained from the National Institutes of Health, Bethesda, MD, USA 20892. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmark = yes, strand = all, expected occurrences = 1-, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

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Please replace the paragraph beginning at page 21, line 33, with the following rewritten paragraph:

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A2 --Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described above using the ALIGN-2 sequence comparison computer program. However, % nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from www-ncbi.nlm.nih.gov or otherwise obtained from the National Institutes of Health, Bethesda, MD USA 20892. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmark = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

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